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OM protein - protein search, using sw model

Run on: January 31, 2005, 18:10:30 ; Search time 28 Seconds

Title: US-10-083-768-12  
Perfect score: 85  
Sequence: 1 CADGPTLREWISFC 14

Scoring table: BL05M62  
GapOp 10.0 , Gapext 0.5  
Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : PIR 79:  
1: pir1:  
2: pir2:  
3: pir3:  
4: pir4:  
5: pir5:  
6: pir6:  
7: pir7:  
8: pir8:  
9: pir9:  
10: pir10:  
11: pir11:  
12: pir12:  
13: pir13:  
14: pir14:  
15: pir15:  
16: pir16:  
17: pir17:  
18: pir18:  
19: pir19:  
20: pir20:  
21: pir21:  
22: pir22:  
23: pir23:  
24: pir24:  
25: pir25:  
26: pir26:  
27: pir27:  
28: pir28:  
29: pir29:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	45	52.9	108	2 T19731	hypothetical protein B24B19.30
2	44	51.8	974	2 S34189	starch phosphoryla
3	44	51.8	1022	1 S00503	Na+/K+-exchanging
4	44	51.8	1023	2 A24414	Na+/K+-exchanging
5	43	50.6	245	2 T47701	translocation initia
6	43	50.6	490	2 T09084	phosphatidylinosit
7	43	50.6	1010	2 B37227	Na+/K+-exchanging
8	43	50.6	1013	1 S00803	Na+/K+-exchanging
9	43	50.6	1013	2 C24639	Na+/K+-exchanging
10	43	50.6	1017	2 A37227	Na+/K+-exchanging
11	43	50.6	1020	2 A34474	Na+/K+-exchanging
12	43	50.6	1020	2 B24639	Na+/K+-exchanging
13	43	50.6	1021	1 PMSHNA	Na+/K+-exchanging
14	43	50.6	1021	1 S04630	Na+/K+-exchanging
15	43	50.6	1021	2 A28199	Na+/K+-exchanging
16	43	50.6	1021	2 B24862	Na+/K+-exchanging
17	43	50.6	1022	2 S49127	Na+/K+-exchanging
18	43	50.6	1023	1 A24639	Na+/K+-exchanging
19	43	50.6	1023	1 S24650	Na+/K+-exchanging
20	43	50.6	1025	2 A60444	Na+/K+-exchanging
21	43	50.6	1027	1 PNCNM	Na+/K+-exchanging
22	43	50.6	1038	1 S03632	Na+/K+-exchanging
23	42.5	50.0	1004	2 JH0470	Na+/K+-exchanging
24	42.5	49.4	312	2 F86876	hypothetical protein
25	42	49.4	522	2 D69226	probable membrane
26	42	49.4	522	2 S22941	conserved hypothetical
27	42	49.4	725	2 A11544	starch phosphoryla
28	42	49.4	842	2 T12091	hypothetical protein
29	41	48.2	189	2 S07755	

hypothetical protein B24B19.30 [Imported] - Neurospora crassa

C;Species: Neurospora crassa

C;Date: 02-Jun-2000 #sequence\_revision 02-Jun-2000 #text\_change 18-Aug-2000

C;Accession: T49731

R;Schulte, U.; Aign, V.; Hohiesel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura, A;Reference number: Z25022

A;Accession: T49731

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-108 <SCH>

A;Cross-references: EMBL:AL356192; GSPDB:GN00116; NCSP:B24B19.30

A;Experimental source: BAC clone B24B19; strain OR74A

C;Genetics:

A;Gene: NCSP:B24B19.30

A;Map position: 6

C;Superfamily: Neurospora crassa hypothetical protein B24B19.30

RESULT 1  
T49731

hypothetical protein B24B19.30 [Imported] - Neurospora crassa

C;Species: Neurospora crassa

C;Date: 02-Jun-2000 #sequence\_revision 02-Jun-2000 #text\_change 18-Aug-2000

C;Accession: T49731

R;Schulte, U.; Aign, V.; Hohiesel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura, A;Reference number: Z25022

A;Accession: T49731

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-108 <SCH>

A;Cross-references: EMBL:AL356192; GSPDB:GN00116; NCSP:B24B19.30

A;Experimental source: BAC clone B24B19; strain OR74A

C;Genetics:

A;Gene: NCSP:B24B19.30

A;Map position: 6

C;Superfamily: Neurospora crassa hypothetical protein B24B19.30

Query Match 52.9%  
Best Local Similarity 50.0%  
Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Query 1 CADGPTLREWISFC 14  
Db 70 CQCQPTLRLNWLSCW 83

RESULT 2  
S34189

starch phosphorylase (EC 2.4.1.1) L - Potato

C;Species: Solanum tuberosum (potato)

C;Date: 03-Mar-1994 #sequence\_revision 10-Nov-1995 #text\_change 09-Jul-2004

C;Accession: S53489; S34189

R;Sonnewald, U.; Basner, A.; Greve, B.; Steup, M.

Plant Mol. Biol. 27: 567-576, 1995

A;Title: A second L-type isotype of potato glucan phosphorylase: cloning, antisense inhi

A;Reference number: S53489; PMID:9520149;

A;Accession: S53489

A;Status: nucleic acid sequence not shown

A;Molecule type: mRNA

A;Residues: 1-974 <S02>

A;Cross-references: UNIPROT: P53535; EMBL:X73684; PID:9313348; PID:93133

C;Superfamily: Glucan phosphorylase

C;Keywords: glycosyltransferase; hexosyltransferase; phosphoprotein; pyridoxal phosphate

F;820/Binding site: pyridoxal phosphate (Lys) (covalent) #Status predicted

Query Match 51.8%  
Best Local Similarity 58.3%  
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 3 DGPTLREWISFC 14  
: : : : | : |||  
Db 619 NGVTPRRLWSRC 630

RESULT 3  
S00503 Na+/K+-exchanging ATPase (BC 3.6.3.9) alpha chain - Pacific electric ray  
C;Species: Torpedo californica (Pacific electric ray)  
C;Date: 30-Jun-1993 #sequence revision 30-Jun-1993 #text\_change 09-Jul-2004  
C;Accession: S00503; S28885; S29880  
R;Kawakami, K.; Noguchi, S.; Noda, M.; Takahashi, R.; Ohta, T.; Kawamura, M.; Nojima, H.  
Nature 316, 733-736, 1985  
A;Title: Primary structure of the alpha subunit of Torpedo californica (Na(+)+K(+))ATPase  
A;Reference number: S00503; MUID:2993905  
A;Accession: S00503  
A;Molecule type: mRNA  
A;Residues: 1-1022 <KAW1>  
A;Cross-references: UNIPROT:PO5025; EMBL:X02810; NID:964399; PIDN:CAA26578.1; PID:964400  
A;Accession: S28885  
A;Molecule type: protein  
A;Residues: 228-240;311-438;535-550;671-690;1011-1022 <KAW2>  
R;Ohta, T.; Nogano, K.; Yoshiida, M.  
Proc. Natl. Acad. Sci. U.S.A. 83, 2071-2075, 1986  
A;Title: The active site structure of Na(+)/K(+)-transporting ATPase: location of the 5'-  
A;Reference number: S29880; MUID:86177549; PMID:3008150  
A;Accession: S29880  
A;Molecule type: protein  
A;Residues: 386-402;502-512;671-689;887-906 <OHT>  
C;Superfamily: Na+/K+-transporting ATPase alpha chain; ATPase nucleotide-binding domain  
C;Keywords: ATP; heterodimer; hydrolase; ion transport; phosphoprotein; potassium trans  
F:56-120/Domain: transmembrane #status predicted <TM1>  
F:130-149/Domain: transmembrane #status predicted <TM1>  
F:150-280/Domain: intracellular #status predicted <INT1>  
F:6-95/Domain: transmembrane #status predicted <TM1>  
F:130-149/Domain: transmembrane #status predicted <TM1>  
F:291-313/Domain: transmembrane #status predicted <TM3>  
F:320-348/Domain: transmembrane #status predicted <TM4>  
F:349-786/Domain: intracellular #status predicted <INT3>  
F:587-783/Domain: ATPase nucleotide-binding domain homology <ATN>  
F:787-810/Domain: transmembrane #status predicted <TM5>  
F:849-874/Domain: transmembrane #status predicted <TM6>  
F:855-932/Domain: intracellular #status predicted <INT4>  
F:933-978/Domain: transmembrane #status predicted <TM7>  
F:979-1023/Domain: extracellular #status predicted <EXT>  
F:376/Active site: Asp (aspartyl)phosphate intermediate) #status predicted  
F:508/Binding site: Asp (lys) #status predicted  
F:717,721,726/Active site: Asp, Asp, Lys #status predicted

Query Match 51.8% Score 44; DB 1; Length 1022;  
Best Local Similarity 70.0% Pred. No. 45;  
Matches 7; Conservative 3; Indels 0; Gaps 0; Gaps 0;  
Qy 5 PTLEWISFC 14  
Db 84 PTPEWIKFC 93

## RESULT 4

A24414 Na+/K+-exchanging ATPase (BC 3.6.3.9) alpha-1 chain - human  
N;Alternate names: sodium pump; sodium/potassium transporting ATPase alpha-A chain  
C;Species: Homo sapiens (man)  
C;Date: 02-Jun-1988 #sequence\_revision 02-Jun-1988 #text\_change 09-Jul-2004  
C;Accession: A24414; A27795; A3910; I60116; S09171  
R;Kawakami, K.; Ohta, T.; Nojima, H.; Nagano, K.  
J. Biochem. 100, 389-397, 1986  
A;Title: Primary structure of the alpha-subunit of human Na<sub>x</sub>K-ATPase deduced from cDNA  
A;Reference number: A24414; MUID:87057096; PMID:2430951  
A;Accession: A24414  
A;Molecule type: mRNA  
A;Residues: 1-1023 <KAW1>  
A;Cross-references: UNIPROT:P05023; EMBL:X04297; NID:928926; PIDN:CAA27840.1; PID:98927  
R;Shull, M.M.; Lingrel, J.B.  
Proc. Natl. Acad. Sci. U.S.A. 84, 4039-4043, 1987

## RESULT 5

T47701 translation initiation factor eIF-6-like protein [Imported] - *Arabidopsis thaliana*  
N;Alternate names: Protin F116.30  
C;Species: *Arabidopsis thaliana* (mouse-ear cress)  
C;Date: 20-Apr-2000 #sequence\_revision 20-Apr-2000 #text\_change 09-Jul-2004  
C;Accession: T47701  
R;Benes, V.; Wurmback, B.; Drzonek, H.; Anserge, W.; Newes, H.W.; Lemcke, K.; Mayer, K.F.  
submitted to the Protein Sequence Database, March 2000  
A;Reference number: Z24473  
A;Accession: T47701  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residue: 1-245 <KAW1>  
A;Cross-references: UNIPROT:Q9M060; EMBL:ALI61667  
A;Experiment source: cultivar Columbia; BAC clone F116  
C;Genetics:

A; Map position: 3  
 A; Introns: 4/1; 36/2; 65/1; 80/1; 123/3; 160/3  
 A; Note: F116.30  
 C; Superfamily: conserved hypothetical protein YPR016C

Query Match 50.6%; Score 43; DB 2; Length 245;  
 Best Local Similarity 53.8%; Pred. No. 17;  
 Matches 2; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 2 ADGPTURBWWISFC 14  
 Db 194 AAGMTVNDWTSFC 206

RESULT 6  
 T09084 phosphatidylinositol 3-kinase - Chlamydomonas reinhardtii (fragment)  
 C;Species: Chlamydomonas reinhardtii  
 C;Accession: T09084  
 C;Sequence\_revision: 11-Jun-1999 #text\_change 09-Jul-2004  
 A;Reference number: 216411; MUID:96281574; PMID:9620264  
 A;Status: preliminary; translated from GB/EMBL/DBJ  
 A;Molecule type: DNA  
 A;Residues: 1-90 <MOL>  
 A;Cross-references: UNIPROT:004270; EMBL:U97663; NID:92109290; PIDN: AAC50018.1; PID:92109290; PIDN: AAC50018.1; PID:92109290  
 A;Experimental source: strain cw-15  
 C;Genetics: A;Introns: 265/3; 331/3; 370/3; 455/1; 481/3  
 A;Molecule type: RNA  
 A;Residues: 243-434 <SVB2>  
 A;Cross-references: GB:M27570  
 C;Genetics:

Query Match 50.6%; Score 43; DB 2; Length 490;  
 Best Local Similarity 57.1%; Pred. No. 32;  
 Matches 2; Conservative 2; Mismatches 2; Indels 2; Gaps 1;

Qy 3 DGPTLR--EWISFC 14  
 Db 250 DGSTARWDNLTCF 263

RESULT 7  
 B37227 Na+/K+-exchanging ATPase (EC 3.6.3.9) alpha-3 chain - chicken  
 C;Species: Gallus gallus (chicken)  
 C;Accession: B37227; I50395  
 C;Sequence\_revision: 16-Sep-1992 #text\_change 09-Jul-2004  
 R;keyeay, K.; Lemas, V.; Fambrough, D.M.  
 Am. J. Physiol. 259, C619-C630, 1990  
 A;Title: Stability of Na(+)-K(+)-ATPase alpha-subunit isoforms in evolution.  
 A;Reference number: A37227; MUID:91023019; PMID:2171348  
 A;Molecule type: mRNA  
 A;Residues: 1-1010 <TA2>  
 A;Cross-references: UNIPROT:P24798; GB:MS960; PID:9212407; PIDN: AAA46982.1; PID:9212408  
 C;Superfamily: Na+/K+-transporting ATPase alpha chain, ATPase nucleotide-binding domain  
 C;Keywords: ATP; Glycoprotein; hydrolase; phosphoprotein; potassium transport; sodium transport  
 F;57-770/Domain: ATPase nucleotide-binding domain homology <ATN>  
 F;203-470/Binding site: carbohydrate (Asn) (covalent) #status predicted  
 F;365/Active site: Asp (aspartyl)phosphate intermediate #status predicted  
 F;495/Binding site: ATP (Lys) #status predicted

Query Match 50.6%; Score 43; DB 2; Length 1010;  
 Best Local Similarity 60.0%; Pred. No. 64;  
 Matches 1; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 5 PTLRENTISFC 14  
 Db 71 PTTPEWVKFC 83

RESULT 9  
 C24439 Na+/K+-exchanging ATPase (EC 3.6.3.9) alpha-3 chain - rat  
 N;Alternate names: Na+/K+-transporting ATPase alpha (III) chain  
 C;Species: Rattus norvegicus (Norway rat)  
 C;Accession: C24439; S00514; B27180; A60470  
 C;Cross-references: UNIPROT:004270; EMBL:U97663; NID:92109290; PIDN: AAC50018.1; PID:92109290  
 C;Sequence\_revision: 23-Apr-1993 #text\_change 09-Jul-2004

R;Shull, G.E.; Green, J.; Lingrel, J.B.  
 A;Title: Molecular cloning of three distinct forms of the Na<sup>+</sup>,K<sup>+</sup>-ATPase alpha-subunit for  
 A;Reference number: A90512; MUID:3028408; PMID:3028400  
 A;Accession: C24639  
 A;Molecule type: mRNA  
 A;Residues: 1-1013 <SHU>  
 A;Cross-references: UNIPROT:PO06687; EMBL:MI4513; PIDN:AAA04777.1; PID:90300  
 A;Note: In the authors' translation 405-Ser is shown after residue 409 and, consequently  
 R;Fara, Y.; Urayama, K.; Nojima, H.; Nagamune, H.; Ohta, T.; N  
 J. Biochem. 10, 3-58, 1987  
 A;Title: Primary structures of two types of alpha-subunit of rat brain Na<sup>+</sup>,K<sup>+</sup>-ATPase  
 A;Reference number: S00460; MUID:88032933; PMID:2822682  
 A;Molecule type: mRNA  
 A;Residues: 1-907, 'C', 909-1013 <HAR>  
 A;Cross-references: EMBL:05883; PID:955769; PIDN:CAA29307.1; PID:955770  
 R;Herrera, V.L.M.; Emanuel, J.R.; Ruiz-Opazo, N.; Levenson, R.; Nadal-Ginard, B.  
 J. Cell Biol. 105, 1855-1865, 1987  
 A;Title: Three differentially expressed Na<sup>+</sup>,K<sup>+</sup>-ATPase alpha subunit isoforms: structural and functional analysis  
 A;Accession: B27180  
 A;Molecule type: mRNA  
 A;Residues: 1, 'NL', 4-103, 'R', 105-113, 'E', 115-127, 'G', 129-148, 'Q', 150-151, 'T', 153-165, 'D'  
 A;Cross-references: EMBL:W28648; PIDN:g205633; PIDN:AAA41672.1; PID:920534  
 A;Note: The authors translated the codon CAG for residue 149 as Glu, GGC for residue 194  
 R;Hsu, Y.M.; Guidotti, G.  
 Biochemistry 28, 569-573, 1989  
 A;Title: Rat brain has the alpha3 form of the (Na<sup>+</sup>,K<sup>+</sup>)ATPase.  
 A;Reference number: A60470; MUID:89229049; PMID:2540801  
 A;Accession: A60470  
 A;Molecule type: protein  
 A;Residues: 117-112; 586-595, 'X', 597-601 <HSU>  
 C;Comment: The alpha-3 form appears to be highly ouabain-inhibitable, as is alpha-2 but  
 C;Genetics:  
 A;Gene: NRKAA3  
 C;Superfamily: Na<sup>+</sup>/K<sup>+</sup>-transporting ATPase alpha chain; ATPase nucleotide-binding domain  
 C;Keywords: ATP; heterodimer; hydrolase; ion transport; phosphoprotein; potassium transp  
 F;86-110/Domain: transmembrane #status predicted <TM1>  
 F;120-139/Domain: transmembrane #status predicted <TM2>  
 F;140-280/Domain: intracellular #status predicted <INT2>  
 F;281-303/Domain: transmembrane #status predicted <TM3>  
 F;310-338/Domain: transmembrane #status predicted <TM4>  
 F;339-776/Domain: intracellular #status predicted <INT3>  
 F;777-800/Domain: ATPase nucleotide-binding domain #status predicted <ATN>  
 F;869-864/Domain: transmembrane #status predicted <TM6>  
 F;943-942/Domain: intracellular #status predicted <INT4>  
 F;959-1013/Domain: extracellular #status predicted <TM7>  
 F;366/Active site: Asp (Lys) #status predicted <EXT>  
 F;498/Binding site: ATP (Lys) #status predicted <EXT>  
 F;707,711,716/Active site: Asp, Asp, Lys #status predicted  
 Query Match Score 43; DB 2; Length 1013;  
 Best Local Similarity 60.0%; Pred. No. 64;  
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
 QY 5 PTLEWISFC 14  
 DB 74 PTPEWVFC 83

RESULT 11

A;Accession: I50394  
 A;Status: preliminary; translated from GB/EMBL/DDBJ  
 A;Molecule type: mRNA  
 A;Residues: 1-1017 <TAK>  
 A;Cross-references: UNIPROT:P24797; GB:MS5959; PIDN:AAA48981.1; PID:9212406  
 R;Takeyau, K.; Lemas, V.; Fambrough, D.M.  
 Am. J. Physiol. 259, C619-C630, 1990  
 A;Title: Stability of Na<sup>+</sup>,K<sup>+</sup>-ATPase alpha-subunit isoforms in evolution.  
 A;Reference number: A37227; MUID:91023019; PMID:2171148  
 A;Accession: A37227  
 A;Molecule type: mRNA  
 A;Residues: 3-1017 <TA2>  
 C;Superfamily: Na<sup>+</sup>,K<sup>+</sup>-transporting ATPase alpha chain; ATPase nucleotide-binding domain  
 C;Keywords: ATP; glycoprotein; hydrolase; phosphoprotein  
 F;1581-1777/Domain: ATPase nucleotide-binding domain homology <ATN>  
 F;210,478/Binding site: carbohydrate (Asn) (covalent) #status predicted  
 F;371/Active site: Asp (aspartylphosphate intermediate) #status predicted  
 Query Match Score 43; DB 2; Length 1017;  
 Best Local Similarity 60.0%; Pred. No. 64;  
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
 QY 5 PTLEWISFC 14  
 DB 79 PTPEWVFC 88

RESULT 12

A;Accession: I50394  
 A;Status: preliminary; translated from GB/EMBL/DDBJ  
 A;Molecule type: mRNA  
 A;Residues: 1-1017 <SHU>  
 A;Cross-references: UNIPROT:P50993; GB:J05096; PIDN:9179164; PID:9179165  
 N;Alternate names: Na<sup>+</sup>/K<sup>+</sup>-exchanging ATPase alpha chain-4; sodium/potassium transporting  
 C;Species: Homo sapiens (man)  
 C;Accession: A34474; B27795; D27397  
 C;Accession: A34474; B27795; D27397  
 R;Shull, M.M.; Lingrel, J.B.  
 Proc. Natl. Acad. Sci. U.S.A. 84, 4039-4043, 1987  
 A;Title: Multiple genes encode the human Na<sup>+</sup>,K<sup>+</sup>-ATPase catalytic subunit.  
 A;Reference number: A34474; MUID:90008924; PMID:247373  
 A;Accession: A34474  
 A;Molecule type: DNA  
 A;Residue: 1-1020 <SHU>  
 A;Cross-references: UNIPROT:P50993; GB:J05096; PIDN:9179164; PID:9179165  
 A;Cross-references: UNIPROT:P50993; GB:J05096; PIDN:9179164; PID:9179165  
 A;Map position: 1q21-1q23  
 C;Keywords: ATP; heterodimer; hydrolase; ion transport; phosphoprotein; potassium transp  
 F;6-1020/Product: Na<sup>+</sup>/K<sup>+</sup>-transporting ATPase alpha chain #status predicted <ATN>  
 F;6-93/Domain: intracellular #status predicted <INT1>  
 F;94-118/Domain: transmembrane #status predicted <TM1>  
 F;128-147/Domain: intracellular #status predicted <TM2>  
 F;148-288/Domain: intracellular #status predicted <INT2>  
 F;289-311/Domain: transmembrane #status predicted <TM3>  
 F;318-346/Domain: transmembrane #status predicted <TM4>  
 F;347-783/Domain: intracellular #status predicted <INT3>  
 A;Reference number: A34474

RESULT 10

A;Accession: I50394  
 A;Status: preliminary; translated from GB/EMBL/DDBJ  
 A;Molecule type: mRNA  
 A;Residues: 1-1017 <TAK>  
 A;Cross-references: UNIPROT:P24797; GB:MS5959; PIDN:AAA48981.1; PID:9212406  
 R;Takeyau, K.; Lemas, V.; Fambrough, D.M.  
 Am. J. Physiol. 259, 619-630, 1990  
 A;Title: Stability of the Na<sup>+</sup>,K<sup>+</sup>-ATPase alpha-subunit isoforms in evolution.  
 A;Reference number: I50394

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>RPSBHA
 584-780/Domain: ATPase nucleotide-binding domain homology <ATN>
  F;872-971/Domain: transmembrane #status predicted <TM5>
  F;872-949/Domain: intracellular #status predicted <INT6>
  F;950-975/Domain: transmembrane #status predicted <TM7>
  F;976-1020/Domain: extracellular #status predicted <EXT>
  F;374/Active site: Asp (aspartylphosphate intermediate) #status predicted
  F;505/Binding site: ATP (Lys) #status predicted
  F;714,718,723/Active site: Asp, Asp, Lys #status predicted

Query Match Score 43; DB 2; Length 1020;
Best Local Similarity 60.0%; Pred. No. 65; 0;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
Qy 5 PTLRWISFC 14
  | | |: |
  82 PTTPEWKFC 91

>RESULT 12
B246339
  B246339 Na+/K+-exchanging ATPase (EC 3.6.3.9) alpha-2 chain - rat
  C;Species: Rattus norvegicus (Norway rat)
  C;Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 09-Jul-2004
  C;Accession: B246339
  R;Shull, G.E.; Green, J.; Lingrel, J. B.
  Biochemistry 25, 8125-8132, 1986
  A;Title: Molecular cloning of three distinct forms of the Na+,K+-ATPase alpha-subunit f
  A;Reference number: A90512; PMID:87128908; PMID:3028470
  A;Accession: B246339
  A;Molecule type: mRNA
  A;Cross-references: UNIPROT:P06686; EMBL:MI14512; NID:9203028; PIDN:AAA40776.1; PID:9203
  C;Gene IDs:
  A;Gene: NKA2
  C;Superfamily: Na+/K+-transporting ATPase alpha chain; ATPase nucleotide-binding domain
  C;Keywords: ATP; heterodimer; hydrolase; ion transport; phosphoprotein; potassium trans-
  F;6-1020/Product: Na+/K+-transporting ATPase alpha-2 chain #status predicted <MAT>
  F;6-93/Domain: intracellular #status predicted <INT1>
  F;9-11/Domain: transmembrane #status predicted <TM1>
  F;14-28/Domain: transmembrane #status predicted <TM2>
  F;148-289/Domain: intracellular #status predicted <INT2>
  F;289-346/Domain: transmembrane #status predicted <TM3>
  F;318-346/Domain: transmembrane #status predicted <TM4>
  F;347-783/Domain: intracellular #status predicted <INT3>
  F;784-780/Domain: ATPase nucleotide-binding domain homology <ATN>
  F;84-807/Domain: transmembrane #status predicted <TM5>
  F;84-871/Domain: transmembrane #status predicted <TM6>
  F;872-949/Domain: intracellular #status predicted <INT7>
  F;950-975/Domain: transmembrane #status predicted <TM8>
  F;976-1020/Domain: extracellular #status predicted <EXT>
  F;374/Active site: Asp (aspartylphosphate intermediate) #status predicted
  F;505/Binding site: ATP (Lys) #status predicted
  F;714,718,723/Active site: Asp, Asp, Lys #status predicted

Query Match Score 43; DB 2; Length 1020;
Best Local Similarity 60.0%; Pred. No. 65; 0;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
Qy 5 PTLRWISFC 14
  | | |: |
  82 PTTPEWKFC 91

>RESULT 13
PNSBHA
  584-780/Domain: Na+/K+-exchanging ATPase (EC 3.6.3.9) alpha chain precursor - sheep
  C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
  C;Accession: A01074; A23426
  R;Shull, G.E.; Schwartz, A.; Lingrel, J. B.


```

Nature 316, 691-695, 1985  
 A:Title: Amino-acid sequence of the catalytic subunit of the  $\text{Na}^+(\text{+})\text{ATPase}$  deduced  
 A:Reference number: A01074; MUID:85296299; PMID:2993903  
 A:Accession: A01074  
 A:Molecule type: mRNA  
 A:Residues: 1-1021 <SH>  
 A:Cross-references: UNIPROT: P04074; GB:X02813; NID:91205; PID:CAA26581.1; PID:91206  
 A:Hinz, H.R.; Kirley, T.L.  
 J. Biol. Chem. 265, 10260-10265, 1990  
 A:Title: Lysine 480 is an essential residue in the putative ATP site of lamb kidney (Na,  
 A:Reference number: A35426; MUID:90285144; PMID:2162343  
 A:Accession: A35426  
 A:Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 475-492 <HIN>  
 C:Comment: This is the catalytic component of the active enzyme, which catalyzes the hydrolysis of the electrochemical gradient of sodium and potassium, providing the energy for active function.  
 C:Comment: This enzyme is specifically inhibited by cardiac glycosides such as digoxin and ouabain.  
 C:Keywords: ATP; hydrolyase; ATPase nucleotide-binding domain; sodium transport; transmembrane domain;  $\text{Na}^+/\text{K}^+$ -transporting ATPase alpha chain #status predicted <ATN>  
 P:6-1021/Product:  $\text{Na}^+/\text{K}^+$ -transporting ATPase alpha chain #status predicted <ATP>  
 P:94-115/Domain: transmembrane #status predicted <TM1>  
 P:128-144/Domain: transmembrane #status predicted <TM2>  
 P:289-311/Domain: transmembrane #status predicted <TM3>  
 P:318-346/Domain: transmembrane #status predicted <TM4>  
 P:585-581/Domain: ATPase nucleotide-binding domain homology <ATN>  
 P:785-808/Domain: transmembrane #status predicted <TM5>  
 P:847-872/Domain: transmembrane #status predicted <TM6>  
 P:951-976/Domain: transmembrane #status predicted <TM7>  
 P:315/Binding site: cardiac glycoside (I- $\text{P}_i$ ) #status predicted  
 P:374/Active site: ATP (aspartate intermediate) #status predicted  
 P:506/Binding site: ATP (aspartate intermediate) #status predicted

F;951-976/Domain: transmembrane #status predicted <TM7>  
 F;977-1021/Domain: extracellular #status predicted <EXT>  
 P;J374/Active site: Asp (aspartylphosphate intermediate) #status predicted  
 F;506/Binding site: ATP (Lys) #status predicted  
 F;715,719,724/Active site: Asp, Asp, Lys #status predicted  
  
 Query Match 50.6%; Score 43; DB 1; Length 1021;  
 Best Local Similarity 60.0%; Pred. No. 65;  
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
  
 Qy 5 PTLEWISFC 14  
 Db 82 PTPEWVKFC 91

RESULT 15  
 A28199  
 Na+/K+-exchanging ATPase (EC 3.6.3.9) alpha chain - chicken  
 C;Species: Gallus gallus (chicken)  
 C;Accession: A28199  
 C;Cross-references: 21-Sep-1988 #sequence\_revision 21-Sep-1988 #text\_change 09-Jul-2004  
 R;Takeyasu, K.; Tamkun, M.M.; Renaud, K.J.; Fambrough, D.M.  
 J. Biol. Chem. 263, 4347-4354, 1988  
 A;Title: Oubain-sensitive (Na<sup>+</sup>) + K<sup>(+)</sup>-ATPase activity expressed in mouse L cells by  
 A;Reference number: A28199; MUID:88153759; PMID:2831227  
 A;Accession: A28199  
 A;Status: preliminary; not compared with conceptual translation  
 A;Molecule type: mRNA  
 A;Residues: 1-1021 <TAK>  
 A;Cross-references: UNIPROT:P09572; GB:J03230; NID:9211219; PID:AAA48607.1; PID:g211220  
 C;Superfamily: Na<sup>+</sup>/K<sup>+</sup>-transporting ATPase alpha chain; ATPase nucleotide-binding domain  
 C;Keywords: ATP; glycoprotein; hydrolase; phosphoprotein; transmembrane protein  
 F;565-781/Domain: ATPase nucleotide-binding domain homology <ATP>  
 F;213-481/Binding site: carbohydrate (An) (covalent) #status predicted  
 F;J374/Active site: Asp (aspartylphosphate intermediate) #status predicted  
 F;506/Binding site: Asp (Lys) #status predicted  
  
 Query Match 50.6%; Score 43; DB 2; Length 1021;  
 Best Local Similarity 60.0%; Pred. No. 65;  
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
  
 Qy 5 PTLEWISFC 14  
 Db 82 PTPEWVKFC 91

Search completed: January 31, 2005, 18:22:36  
 Job time : 30 secs